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DB=PG	PB, USPT, EPAB, JPAB, DWPI, TDBD; PLUR=YES; OP=OR	
L21	L19 and threshold	216
L20	L19 and negative near match	0
L19	L18 and match and mismatch	· 283
L18	L17 and error same (rate or association)	410
L17	L16 and sequence adj alignment	6496
L16	first same sequence and second same sequence and percent adj identity	10717
L15	L14 and error same (associate or associating or association)	7
L14	L13 and percent adj identity	1823
L13	pairwise adj alignment	2680
· L12	L11 and sequence same alignment	4
L11	kristof.in.	333
L10	kristofi.in.	0
L9	L8 and sequence same alignment	5
L8	heus.in.	136
L7	L6 and sequence same alignment	3
L6	glemet.in.	33
L5	L4 and sequence same alignment	5
L4	duval.in.	1429
L3	L2 and sequence same alignment	5
L2	dufresne.in.	756
L1	codani.in.	4
	DB=PG L21 L20 L19 L18 L17 L16 L15 L14 L13 L12 L11 L10 L9 L8 L7 L6 L5 L4 L3 L2	DB=PGPB, USPT, EPAB, JPAB, DWPI, TDBD; PLUR=YES; OP=OR L21 L19 and threshold L20 L19 and negative near match L19 L18 and match and mismatch L18 L17 and error same (rate or association) L17 L16 and sequence adj alignment L16 first same sequence and second same sequence and percent adj identity L15 L14 and error same (associate or associating or association) L14 L13 and percent adj identity L13 pairwise adj alignment L12 L11 and sequence same alignment L11 kristof.in. L10 kristofi.in. L9 L8 and sequence same alignment L8 heus.in. L7 L6 and sequence same alignment L6 glemet.in. L5 L4 and sequence same alignment L4 duval.in. L3 L2 and sequence same alignment L4 dufresne.in.

END OF SEARCH HISTORY